

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	48	27.9	192	6	US-10-981-873-43	Sequence 43, Appl
2	47.5	27.6	3674	7	US-11-000-463-454	Sequence 454, App
3	46	26.7	334	6	US-10-793-626-282	Sequence 282, App
4	45.5	26.5	750	7	US-11-133-285-2	Sequence 2, Appl
5	45.5	26.5	1001	7	US-11-133-285-40	Sequence 40, Appl
6	45.5	26.5	1013	6	US-10-131-836A-38	Sequence 38, Appl
7	44.5	25.9	662	7	US-11-090-439-9	Sequence 9, Appl
8	44	25.6	407	7	US-11-127-877-56	Sequence 56, Appl
9	44	25.6	573	6	US-10-525-710-36	Sequence 36, Appl
10	43.5	25.3	218	6	US-10-793-626-562	Sequence 562, App
11	43.5	25.3	792	7	US-11-108-172-1127	Sequence 1127, Ap
12	43	25.0	192	7	US-11-053-822-206	Sequence 206, App
13	43	25.0	192	7	US-11-053-822-250	Sequence 250, App
14	43	25.0	200	7	US-11-055-822-204	Sequence 204, App
15	43	25.0	200	7	US-11-055-822-248	Sequence 248, App
16	43	25.0	275	7	US-11-107-028-23	Sequence 23, Appl
17	43	25.0	437	6	US-10-858-730-214	Sequence 214, App
18	43	25.0	437	6	US-10-858-730-283	Sequence 283, App
19	43	25.0	437	6	US-10-858-730-288	Sequence 288, App
20	43	25.0	480	6	US-10-510-386-12	Sequence 12, Appl
21	43	25.0	841	7	US-11-052-554A-102	Sequence 102, App
22	43	25.0	873	6	US-10-793-626-3036	Sequence 3036, Ap
23	43	25.0	1070	7	US-11-000-463-721	Sequence 721, App
24	43	25.0	1194	7	US-11-000-463-249	Sequence 249, App
25	42	24.4	684	6	US-10-714-781A-55	Sequence 55, Appl

ALIGNMENTS

```

RESULT 1
US-10-981-873-43
; Sequence 43, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981.873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-981-873-43

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Query Match      27.9%;   Score 48;   DB 6;   Length 192;
Best Local Similarity 53.3%;   Pred. No. 3.5;
Matches 8;   Conservative .. 1;   Mismatches 6;   Indels 0;   Gaps 0;

QY      7  LETRTETWMSSEGAW 21
          |||||
          :|
          :|
          :|
          :|

Db      129  LETRLADWIHSSGGW 143

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RESULT 2
US-11-000-463-454
; Sequence 454, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:38:57 ; Search time 164 Seconds
(without alignments)
76.432 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	30	3	US-09-881-710-3
2	172	100.0	30	3	US-09-881-710-11
3	172	100.0	30	4	US-10-634-895-3
4	172	100.0	30	4	US-10-634-895-11
5	172	100.0	40	5	US-10-608-147-31
6	172	100.0	48	4	US-10-311-213-32
7	172	100.0	48	5	US-10-608-029-35
8	172	100.0	685	5	US-10-500-796A-43
9	172	100.0	685	5	US-10-500-796A-45
10	172	100.0	685	5	US-10-500-796A-47
11	168	97.7	40	3	US-09-881-710-29
12	168	97.7	40	4	US-10-634-895-29
13	168	97.7	167	4	US-10-375-932-122
14	168	97.7	171	4	US-10-375-932-118
15	168	97.7	171	4	US-10-375-932-121
16	168	97.7	675	4	US-10-375-932-143
17	168	97.7	677	4	US-10-375-932-238
18	168	97.7	681	4	US-10-375-932-142
19	168	97.7	681	4	US-10-375-932-228
20	168	97.7	1127	4	US-10-247-960-3
21	168	97.7	3388	5	US-10-719-547-17
22	168	97.7	3391	5	US-10-719-547-21
23	168	97.7	3391	5	US-10-871-775-31
24	163	94.8	678	4	US-10-375-932-248
25	162	94.2	661	5	US-10-701-122-51
26	160	93.0	40	4	US-10-311-213-3
27	160	93.0	677	4	US-10-375-932-345

28 159 92.4 675 4 US-10-375-932-237 Sequence 237, App
29 159 92.4 675 4 US-10-375-932-240 Sequence 240, App
30 159 92.4 675 4 US-10-375-932-241 Sequence 241, App
31 159 92.4 675 4 US-10-375-932-243 Sequence 243, App
32 159 92.4 675 4 US-10-375-932-243 Sequence 251, App
33 159 92.4 675 4 US-10-375-932-243 Sequence 252, App
34 159 92.4 677 4 US-10-375-932-242 Sequence 242, App
35 157.5 91.6 39 5 US-10-608-029-23 Sequence 23, Appl
36 157.5 91.6 39 5 US-10-608-029-29 Sequence 29, Appl
37 156 90.7 35 4 US-10-311-213-13 Sequence 13, Appl
38 156 90.7 39 3 US-09-881-710-12 Sequence 12, Appl
39 156 90.7 39 4 US-10-634-895-12 Sequence 12, Appl
40 156 90.7 40 3 US-09-881-710-28 Sequence 28, Appl
41 156 90.7 40 4 US-10-634-895-28 Sequence 28, Appl
42 156 90.7 40 4 US-10-311-213-1 Sequence 1, Appl
43 156 90.7 40 4 US-10-311-213-20 Sequence 20, Appl
44 156 90.7 40 5 US-10-608-147-38 Sequence 38, Appl
45 156 90.7 76 3 US-09-881-710-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-881-710-3
; Sequence 3, Application US/09881710
; Publication No. US20020086403A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671USO
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Dengue virus
US-09-881-710-3

Query Match 100.0%; Score 172; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.7e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30
Db 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30

RESULT 2

US-09-881-710-11
; Sequence 11, Application US/09881710
; Publication No. US20020086403A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671USO
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:38:36 ; Search time 47 Seconds
(without alignments)
52.772 Million cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

- 1: Issued Patents AA:**
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- 3: /cgn2_6/ptodata/1/iaa/6.COMB.pep:**
- 4: /cgn2_6/ptodata/1/iaa/H.COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/RE.COMB.pep:**
- 7: /cgn2_6/ptodata/1/iaa/backfiles.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	30	2	US-09-881-710-3
2	172	100.0	30	2	US-09-881-710-11
3	168	97.7	40	2	US-09-881-710-29
4	168	97.7	635	2	US-09-341-833A-7
5	168	97.7	677	2	US-09-341-833A-8
6	168	97.7	1127	2	US-08-937-195-3
7	168	97.7	1127	2	US-08-937-195-3
8	168	97.7	1127	2	US-09-376-463-3
9	168	97.7	1127	4	PCT-US96-07627-3
10	162	94.2	661	2	US-09-452-638-51
11	162	94.2	661	2	US-09-121-587A-2
12	156	90.7	39	2	US-09-881-710-12
13	156	90.7	40	2	US-09-881-710-28
14	156	90.7	76	2	US-09-881-710-1
15	152	88.4	635	2	US-09-341-833A-9
16	140	81.4	39	2	US-09-881-710-30
17	116	67.4	22	2	US-09-341-833A-5
18	107	62.2	20	2	US-09-881-710-15
19	102	59.3	20	2	US-09-881-710-17
20	85	49.4	20	2	US-09-881-710-16
21	53	30.8	140	2	US-09-270-767-47302
22	53	30.8	285	2	US-09-252-991A-25160
23	52.5	30.5	303	2	US-09-372-934-2
24	52.5	30.5	303	2	US-09-766-916-2
25	52.5	30.5	303	2	US-09-766-898-2
26	52.5	30.5	303	2	US-09-637-040C-2
27	52.5	30.5	303	2	US-10-306-249-2

28	52	30.2	104	2	US-08-996-138-24	Sequence 24, Appl
29	52	30.2	104	2	US-09-556-972-24	Sequence 24, Appl
30	52	30.2	207	2	US-08-996-138-23	Sequence 23, Appl
31	52	30.2	207	2	US-09-556-972-23	Sequence 23, Appl
32	52	30.2	309	2	US-08-996-138-22	Sequence 22, Appl
33	52	30.2	309	2	US-09-556-972-22	Sequence 22, Appl
34	52	30.2	521	2	US-08-996-138-20	Sequence 20, Appl
35	52	30.2	521	2	US-09-556-972-20	Sequence 20, Appl
36	52	30.2	541	1	US-08-604-333-2	Sequence 2, Appl
37	52	30.2	541	2	US-09-110-618-2	Sequence 2, Appl
38	52	30.2	541	2	US-09-173-151A-28	Sequence 28, Appl
39	52	30.2	541	2	US-09-578-178-2	Sequence 2, Appl
40	52	30.2	541	2	US-09-577-806-2	Sequence 2, Appl
41	52	30.2	541	2	US-09-621-502-4	Sequence 4, Appl
42	52	30.2	541	2	US-09-949-002-360	Sequence 360, App
43	52	30.2	546	2	US-09-949-002-489	Sequence 489, App
44	50.5	29.4	233	2	US-09-902-540-14590	Sequence 14590, A
45	50	29.1	283	2	US-09-252-991A-22696	Sequence 22696, A

ALIGNMENTS

RESULT 1

US-09-881-710-3
; Sequence 3, Application US/09881710
; Patent No. 6673895
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Phillipe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Dengue virus
US-09-881-710-3

Query Match 100.0%; Score 172; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30
Db 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30

RESULT 2

US-09-881-710-11
; Sequence 11, Application US/09881710
; Patent No. 6673895
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Phillipe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671US0
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:33:21 ; Search time 227 Seconds
(without alignments)
93.242 Million cell updates/sec

Title: US-10-634-895-3

Perfect score: 172

Sequence: 1 PHVGMGLTRTWTMSSEGAKHVQRIETW 30

Scoring table: BLOSUM62

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Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	280	2	Q8Q264_9FLAV
2	172	100.0	280	2	Q8Q265_9FLAV
3	172	100.0	280	2	Q8Q266_9FLAV
4	172	100.0	280	2	Q8Q267_9FLAV
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6	172	100.0	661	2	Q5V188_9FLAV
7	172	100.0	661	2	Q5V189_9FLAV
8	172	100.0	661	2	Q5V190_9FLAV
9	172	100.0	661	2	Q5V191_9FLAV
10	172	100.0	716	2	Q6DUV2_9FLAV
11	172	100.0	757	2	Q5S8P1_9FLAV
12	172	100.0	757	2	Q5S8P2_9FLAV
13	172	100.0	757	2	Q6DUD9_9FLAV
14	172	100.0	763	2	Q5ICU8_9FLAV
15	172	100.0	775	2	Q6G398_9FLAV
16	172	100.0	775	2	Q8QY07_9FLAV
17	172	100.0	3391	1	POLG_DEN26
18	172	100.0	3391	1	POLG_DEN27
19	172	100.0	3391	1	POLG_DEN29
20	172	100.0	3391	2	O09234_DEN26
21	172	100.0	3391	2	O11875_9FLAV
22	172	100.0	3391	2	O58Y67_9FLAV
23	172	100.0	3391	2	O58Y69_9FLAV
24	172	100.0	3391	2	O58Y71_9FLAV
25	172	100.0	3391	2	Q8QR27_9FLAV
26	172	100.0	3391	2	Q91U94_9FLAV
27	172	100.0	3391	2	Q68Y26_9FLAV
28	172	100.0	3391	2	Q9B7P0_9FLAV
29	168	97.7	120	2	Q67424_9FLAV
30	168	97.7	166	2	Q6G346_9FLAV
31	168	97.7	661	2	Q5QIB6_9FLAV

32	168	97.7	661	2	Q5V192_9FLAV	Q5V192 dengue viru
33	168	97.7	661	2	Q5V193_9FLAV	Q5V193 dengue viru
34	168	97.7	661	2	Q5V194_9FLAV	Q5V194 dengue viru
35	168	97.7	661	2	Q5V195_9FLAV	Q5V195 dengue viru
36	168	97.7	661	2	Q5V196_9FLAV	Q5V196 dengue viru
37	168	97.7	745	2	Q6KX9_9FLAV	Q6KX9 dengue viru
38	168	97.7	775	2	Q8JYK8_9FLAV	Q8JYK8 dengue viru
39	168	97.7	775	2	Q8QY62_9FLAV	Q8QY62 dengue viru
40	168	97.7	775	2	Q8QY63_9FLAV	Q8QY63 dengue viru
41	168	97.7	779	2	Q88636_9FLAV	Q88636 dengue viru
42	168	97.7	1127	2	P89531_9FLAV	P89531 dengue viru
43	168	97.7	1127	2	P89532_9FLAV	P89532 dengue viru
44	168	97.7	1127	2	Q66454_9FLAV	Q66454 dengue viru
45	168	97.7	1127	2	Q66455_9FLAV	Q66455 dengue viru

ALIGNMENTS

RESULT 1
Q8Q264_9FLAV
ID Q8Q264_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8Q264;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571640; PubMed=11714970;
RA Uzcategui N.Y., Camacho D., Comach G., Cuello de Uzcategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for in situ virus evolution and recombination.";
RL J. Gen. Virol. 82:2945-2953(2001).
DR EMBL; AF360863; AAL76291.1; -; Genomic_RNA.
DR SMR; Q8Q264; 21-100.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 280 AA; 31846 MW; E889FDD11929CBA7 CRC64;

Query Match 100.0%; Score 172; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PHVGMGLTRTWTMSSEGAKHVQRIETW 30
DB 211 PHVGMGLTRTWTMSSEGAKHVQRIETW 240

RESULT 2
Q8Q265_9FLAV
ID Q8Q265_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8Q265;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:34:31 ; Search time 37 Seconds
(without alignments)
78.014 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	775	2 A48644	polyprotein - deng
2	172	100.0	3391	1 GNVV16	genome polyprotein
3	172	100.0	3391	1 GNVV26	genome polyprotein
4	172	100.0	3391	1 GNVVJA	genome polyprotein
5	168	97.7	166	2 S40144	premembrane protein
6	168	97.7	3391	1 GNVVDP	genome polyprotein
7	168	97.7	3391	2 JS0219	polyprotein - deng
8	162	94.2	665	2 PS0043	genome polyprotein
9	159	92.4	3396	1 A42551	genome polyprotein
10	158	91.9	166	2 S03223	membrane protein -
11	156	90.7	775	2 A47311	polyprotein(C, E,
12	156	90.7	792	2 C32401	genome polyprotein
13	156	90.7	792	2 B32401	genome polyprotein
14	156	90.7	792	2 A32401	genome polyprotein
15	156	90.7	1226	1 GNVVWP	genome polyprotein
16	154	89.5	166	2 S03224	membrane protein -
17	154	89.5	166	2 S03225	membrane protein -
18	152	88.4	773	2 A47666	structural polypro
19	152	88.4	733	1 GNVVDF	genome polyprotein
20	145	84.3	3390	1 GNVVD3	genome polyprotein
21	139	80.8	1127	1 GNVVD2	genome polyprotein
22	68	39.5	1163	1 GNVVY8	genome polyprotein
23	68	39.5	3411	1 GNVVY	genome polyprotein
24	68	39.5	3411	1 GNVVYP	genome polyprotein
25	54.5	31.7	636	2 A87134	methylmalonyl-CoA
26	54	31.4	193	2 T08300	hypothetical prote
27	54	31.4	1127	2 G71274	hypothetical prote
28	53.5	31.1	132	2 F82663	hypothetical prote
29	53	30.8	340	2 C71266	conserved hypothet

30	51	29.7	198	2 S77277	leucyltransferase
31	51	29.7	776	2 A41704	genome polyprotein
32	51	29.7	776	2 B41704	genome polyprotein
33	51	29.7	872	2 JC7380	DNA-directed DNA p
34	50	29.1	305	2 A83340	hypothetical prote
35	50	29.1	664	2 T48258	kinasin-like prote
36	50	29.1	707	2 T02835	long chain fatty a
37	50	29.1	1212	2 B82809	exodeoxyribonuclea
38	49.5	28.8	264	2 E69897	hypothetical prote
39	49.5	28.8	351	2 E84096	hypothetical prote
40	49	28.5	833	2 G75621	arylesterase/monox
41	48.5	28.2	248	2 T14547	beta-fructofuranos
42	48.5	28.2	278	2 T48426	hypothetical prote
43	48.5	28.2	605	2 AG0123	probable antigenic
44	48.5	28.2	626	2 AE0123	conserved hypothet
45	48	27.9	259	2 C82148	

ALIGNMENTS

RESULT 1

A48644
polyprotein - dengue virus type 2 (strain Mexican) (fragment)

C:Species: dengue virus type 2
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004
C:Accession: A48644
R:Ruiz, B.H.; Sanchez, I.; Ortega, G.J.; Lopez, I.; Ortiz-Ortiz, L.
submitted to GenBank, October 1992
A:Description: Nucleotide sequence and deduced amino-acid sequence of the structural pr
A:Reference number: A48644
A:Accession: A48644
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-775 <RUI>
A:Cross-references: UNIPROT:Q66398; UNIPARC:UPI000008EB45; GB:L04561; NID:g323652; PIDN
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein

Query Match 100.0%; Score 172; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PHVGMGLETRTETWMSSEGAKHVQRIETW 30
|||||
DB 211 PHVGMGLETRTETWMSSEGAKHVQRIETW 240

RESULT 2

GNV16

genome polyprotein - dengue virus type 2 (strain 16681)

N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstr

tural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: dengue virus type 2

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004

C:Accession: A42451; A43496; A43763

R:Blak, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; Hem

Virolgy 187, 573-590, 1992

A:Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence

A:Reference number: A42451; MUID:92189532; PMID:1312269

A:Accession: A42451

A:Molecule type: genomic RNA

A:Residues: 1-3391 <BLO>

A:Cross-references: UNIPROT:P29990; UNIPARC:UPI0000131DF5; GB:M84727; GB:M85259; NID:g3

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;

F:1-114/Product: capsid protein C #status predicted <CPC>

F:115-280/Product: membrane-associated protein M precursor #status predicted <MPP>

F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>

F:206-280/Product: membrane-associated protein M #status predicted <MPP>

F:268-284/Domain: transmembrane #status predicted <TM1>

F:281-775/Product: envelope protein E #status predicted <EPE>

F:727-743/Domain: transmembrane #status predicted <TM2>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:32:23 ; Search time 186 Seconds
(without alignments)
70,868 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGNGLFRTTWTMSSEGAKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	48	AAE17433	AAE17433 (95-114)E
2	172	100.0	48	ADW12588	Adw12588 p(95-114)
3	172	100.0	685	ABP57874	ABP57874 Plasmid p
4	172	100.0	685	ABP57876	ABP57876 Plasmid p
5	172	100.0	685	ABP57875	ABP57875 Plasmid p
6	172	100.0	3391	AAW06591	AAW06591 Polypeptide
7	172	100.0	3391	AAW06590	AAW06590 Polypeptide
8	172	100.0	3391	AAE07987	AAE07987 Attenuate
9	172	100.0	3391	AAE07986	AAE07986 Wild-type
10	169	98.3	40	AAE17432	AAE17432
11	168	97.7	167	ADN37497	ADN37497
12	168	97.7	171	ADN37493	ADN37493
13	168	97.7	171	ADN37496	ADN37496
14	168	97.7	635	AAW75410	AAW75410 Fusion pr
15	168	97.7	635	ADN37518	ADN37518 Fusion vi
16	168	97.7	677	AAW75411	AAW75411 Fusion pr
17	168	97.7	677	ADN37613	ADN37613 Fusion vi
18	168	97.7	677	ADN37603	ADN37603 Fusion vi
19	168	97.7	681	ADN37517	ADN37517 Fusion vi
20	168	97.7	1127	AAW09409	AAW09409 Fusion vi
21	168	97.7	1127	AAW05522	AAW05522 Fusion vi
22	168	97.7	1127	ADL98086	ADL98086 Fusion vi
23	168	97.7	1127	ADQ28716	ADQ28716 Fusion vi
24	168	97.7	1127	ADQ28716	ADQ28716 Fusion vi

25	168	97.7	3388	6	AAE35314	Dengue vi
26	168	97.7	3391	8	ADG93314	DEN2 (Ton
27	163	94.8	678	8	ADN37623	Dengue vi
28	162	94.2	150	1	AAE91166	PUD-218 s
29	162	94.2	661	4	AAE84901	Dengue-2
30	160	93.0	677	8	ADN37720	Dengue vi
31	159	92.4	675	8	ADN37628	Dengue vi
32	159	92.4	675	8	ADN37616	Dengue vi
33	159	92.4	675	8	ADN37618	Dengue vi
34	159	92.4	675	8	ADN37612	Dengue vi
35	159	92.4	675	8	ADN37615	Dengue vi
36	159	92.4	675	8	ADN37626	Dengue vi
37	159	92.4	677	8	ADN37617	Dengue vi
38	159	92.4	3396	2	AAE43662	DEN1-S275
39	157.5	91.6	39	9	ADW12576	MI-40/DEN
40	157.5	91.6	39	9	ADW12582	MI-40/DEN
41	157.5	91.6	39	9	ADW12599	MI-40/DEN
42	157	91.3	774	8	ADG93320	DEN1 (Pue
43	157	91.3	775	8	ADG93318	DEN1 (Pue
44	156	90.7	39	5	AAE17440	Dengue vi
45	156	90.7	40	5	AAE17431	Dengue (D

ALIGNMENTS

RESULT 1
AAE17433
ID AAE17433 standard; protein; 48 AA.
XX AAE17433;
AC AAE17433;
XX XX
DT 18-APR-2002 (first entry)
XX XX
DB (95-114)EGFP(206-245)DEN-2 fusion protin.
XX XX
KW Dengue virus; pRM glycoprotein; E glycoprotein; apoptosis; virucide;
KW cancer; flavivirus infection; cytostatic; EGFP; DEN-2 protein;
KW enhanced green fluorescent protein; fusion protein; M ectodomain.
XX XX
OS Dengue virus; 2.
OS Dengue virus; 1.
OS Unidentified.
OS Chimeric.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 13. .44 /note= "Encoded by GTRTC"
XX XX
FN WO200196376-A2.
XX XX
PD 20-DEC-2001.
XX XX
PF 18-JUN-2001; 2001WO-IB001570.
XX XX
PR 16-JUN-2000; 2000US-0212129P.
XX XX
PA (INSP) INST PASTEUR.
XX XX
PI Despres P, Courageot M, Deubel V, Cateau A;
XX XX
DR WPI; 2002-139706/18.
XX XX
DR N-PSDB; AAD27335.
XX XX
PT Novel apoptosis inducing polypeptide fragments of Dengue virus-1 or 2 M
PT protein, useful for inducing apoptosis in a cell of a human patient
PT suffering from cancer or flavivirus infection.
XX XX
PS Claim 42; Fig 11; 45pp; English.
XX XX
CC The invention relates to pro-apoptotic fragments of the Dengue virus
CC (DEN) pRM and E glycoproteins, methods for screening molecules capable of
CC inducing apoptosis and methods of inducing apoptosis in a cell. The